

CLAIMS

We claim:

1. A method for modification of a DNA of a bacterial cell comprising in its genome a first attachment site recognized by a protein with Mx9 integrase activity, comprising introducing a Mx9 transformation system into the cell, said system comprising
 - a) a gene encoding a protein with Mx9 integrase activity protein operably linked to a promoter active in the host cell, and
 - b) a DNA vector comprising a second attachment site recognized by the integrase protein, which may be the same as the first attachment site.
2. The method of claim 1 wherein the cell is *Myxococcus* or *Sorangium*.
3. The method of claim 1 wherein the protein has a sequence at least substantially identical to SEQ ID NO:2.
4. The method of claim 3 wherein the protein has a sequence of SEQ ID NO:2.
5. The method of claim 4 wherein the protein is encoded by a gene comprising the sequence of SEQ ID NO:1.
6. The method of claim 1 wherein said first attachment site comprises SEQ ID NO:5.
7. The method of claim 6 wherein said first attachment site is *attB2*.
8. The method of claim 1 wherein said second attachment site comprises SEQ ID NO:5.

9. The method of claim 3 wherein said first attachment site has been recombinantly introduced into the cell genome.
10. The method of claim 1 wherein said DNA vector further comprises an exogenous gene.
11. The method of claim 10 wherein the exogenous gene is selected from the group consisting of *prpE*, *accA*, *pccB*, *matB*, *matC* and beta-galactosidase genes.
12. The method of claim 6 wherein the first and second attachment sites are comprised of identical sequences.
13. The method of claim 2 wherein the cell is *Myxococcus xanthus*.
14. The method of claim 13 wherein the cell produces an epothilone.
15. The method of claim 14, wherein the epothilone is selected from the group consisting of epothilone C and D.
16. A bacterial host cell produced by the method of claim 10.
17. The cell of claim 16 wherein that produces an epothilone selected from epothilone A, B, C, and D.
18. The cell of claim 17, wherein said exogenous gene is selected from the group consisting of *prpE*, *accA*, *pccB*, *matB* and *matC* genes.